

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/254,600A

Source: 1653

Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1653

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/254,600A

DATE: 05/07/2001

TIME: 17:35:51

Input Set : A:\TPP30566.txt

Output Set: N:\CRF3\05072001\I254600A.raw

Does Not Comply
Corrected Diskette Needed

5 <110> APPLICANT: Cohen, Yarom
 9 <120> TITLE OF INVENTION: Pharmaceutical Composition for the Treatment of Syndrom X of Reaven
 13 <130> FILE REFERENCE: TPP30566
 17 <140> CURRENT APPLICATION NUMBER: 09/254,600A
 19 <141> CURRENT FILING DATE: 1999-03-11
 23 <150> PRIOR APPLICATION NUMBER: PCT/IL97/00301
 25 <151> PRIOR FILING DATE: 1997-10-09
 29 <150> PRIOR APPLICATION NUMBER: IL 119250
 31 <151> PRIOR FILING DATE: 1996-09-12
 35 <150> PRIOR APPLICATION NUMBER: IL 119403
 37 <151> PRIOR FILING DATE: 1996-10-10
 E--> 41 <160> NUMBER OF SEQ ID NOS: 8
 45 <170> SOFTWARE: PatentIn version 3.0

Number of sequences differ:
 - 8 listed
 - 7 shown

ERRORED SEQUENCES

247 <210> SEQ ID NO: 7
 249 <211> LENGTH: 28
 251 <212> TYPE: PRT
 253 <213> ORGANISM: HUMAN
 257 <400> SEQUENCE: 7
 259 Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys Ala Gly
 260 1 5 10 15
 262 Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
 263 20 25
 E--> 267 000

If this is extraneous material, please delete.
 If meant to be a skipped sequence, please
 use this format:

<210> 8
 <400> 8

000

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/07/2001

PATENT APPLICATION: US/09/254,600A

TIME: 17:35:52

Input Set : A:\TPP30566.txt

Output Set: N:\CRF3\05072001\I254600A.raw

L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:41 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (8) Counted (7)